1/24 1456 496 3'UTR, TAA 1351 exon 2 Genomic DNA **cDNA** 646 intron 1 ATG 5'UTR exon 1 1300bp promoter



<u>2/24</u>

			10) 2:			_	
	MOUSE-X1.DNA	1		·		0 4	50	
	HUMAN-X1.DNA	3	ATGAAGCTGG	CTABCTCCT	GTGGCTGAG	T TCTGCCGTC	C TCGCTGCCTG	50
			60	7	CIGGCIGAG		C TTGCCACTTA	50
	MOUSE-X1.DNA	51		•		0 90	0 100 GAGGATGCCA	
	HUMAN-X1.DNA	51	CGGTTTTTT	GTTGTGGGA	ACAACCTGA	TGAGGGGCT	GAGGATGCCA	100
			110	120			AAAGATGAAA	100
	MOUSE-X1.DNA	101			130	140	150 GAGGTGCGAG	
	HUMAN-X1.DNA	101	GAGCAAAGGA	プログラング・プログラング	GCGAGGCTG(AGGGCAGCG	GAGGTGCGAG	150
		_	160	170			GAAATGCGAA	150
	MOUSE-X1.DNA	151				190	200	
,¥Bosz,	HUMAN-X1.DNA	151	GAGGCAGGG	AGTGCCCCTT	CCAGCTCACC	CTGCCCACGC	TGACCATCCA	200
1000			210	220	CCAGGTAAGC		TGACTATTCA	200
	MOUSE-X1.DNA	201				240	250	
: Par	HUMAN-X1.DNA	201	GCTCCCGAAC	CUGCIIGGCA	GCATGGAGGA	GGTGCTCAAA	GAAGTGCGGA	250
			GCTCCCGAAG 260	270				250
L	MOUSE-X1.DNA	251				290	300	
-l	HUMAN-X1.DNA	251	CCCTCAAGGA ACCTCAAGGA	AGCAGTGGAC	AGTCTGAAGA	AATCCTGCCA	GGACTGTAAG	300
F			ACCTCAAGGA 310	ARICGIAAAT	AGTCTAAAGA		AGACTGCAAG	300
اليأيا	MOUSE-X1.DNA	301		320	330	340	350	
9	HUMAN-X1.DNA	301	TTGCAGGCTG	ACGACCATCG	AGATCCCGGC	GGGAATGGAG	GG	350
i a d a			CTGCAGGCTG 360	AIGACAACGG	AGACCCAGGC		TGTTGTTACC	350
.	MOUSE-X1.DNA	351		370	380	390	400	
r.	HUMAN-X1.DNA	351	-AATGGA	CCCCCCCCC	CAGCCGAGGA	CAGTAGAGTC	CAGGAACTGG	400
			CAGTACAGGA 410	GCCCCGGAG	AGGTTGGTGA		AGAGAATTAG	400
J	MOUSE-X1.DNA	401		420	430	440	450	
o O	HUMAN-X1.DNA	401	AGAGTCAGGT	TARCARGUTG	TCCTCAGAGC	TGAAGAATGC	AAAGGACCAG	450
			AGAGTGAGGT 460	TANCAAGCTG		TAAAGAATGC	CAAAGAGGAG	450
	MOUSE-X1.DNA	451		470	480	490	500	
	HUMAN-X1.DNA	451	ATCCAGGGGC ATCAATGTAC	TTCARCORGE	CCTGGAGACG	CTCCATCTGG	TAAATATGAA	500
			ATCAATGTAC 510	FOO	CCTGGAGAAG		TAAATATGAA	500
	MOUSE-X1.DNA	501		520	530	540	550	
	HUMAN-X1.DNA	501	CAACATTGAG	AACTACGTGG	ACAACAAAGT	GGCAAATCTA	ACCGTTGTGG	550
		-	CAACATAGAA . 560	AATTATGTTG	ACAGCAAAGT	GGCAAATCTA	ACATTTGTTG	550
	MOUSE-X1.DNA	551		570	580	590	600	
	HUMAN-X1.DNA	551	TCAACAGTTT	GGATGGCAAG	TGTTCCAAGT	GTCCCAGCCA	AGAACACATG	600
		551	TCAATAGTTT (GATGGCAAA	TGTTCAAAGT	GTCCCAGCCA	AGAACAAATA	600
	MOUSE-X1.DNA		610	620	630	640	650	
	HUMAN-X1.DNA	601	CAGTLACAGC (JGG	• • • • • • • • • •	• • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	650
		301 (CAGTCACGTC (∴AG	• • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •	650

<u>3/24</u>

			1	0 0				
	MOUSE-X2.DNA		_	-			50	
	HUMAN-X2.DNA		TTCBBCSTC	ANTATACAA	A GATTGTTCC	G ACCACTACG	ODAAGGAAGG	50
			61 - 11 - 11 - 11 - 11 - 11 - 11 - 11 -	AATATATAA			AATAGGCAAA	50
	MOUSE-X2.DNA	ς.		- ,,		90	100	
	HUMAN-X2.DNA	5.	AGAAGCAGI	S GGGCCTACAC	AGTTACCCC	r gatcacaga:	A ACAGCAGCTT	100
		•	110	MGACCTACAC	AGTTACACC		ATAGTAGCTT	100
	MOUSE-X2.DNA	101				140	150	
	HUMAN-X2.DNA	101	TCABCTTIAC	TGTGACATGG	AGACCATGG	TGGAGGCTGG	ACGGTGCTGC	150
		203	160	TGTGACATGG	AGACCATGG		ACAGTGCTGC	150
	MOUSE-X2.DNA	151				190	200	
	HUMAN-X2.DNA	151	ACCCACCECT	TGATGGCAGC	ACCAACTTC	CCAGAGAGTG	GAAAGACTAC	200
			210	CGATGGGAGC	ACCAACTICA		GCAAGACTAC	200
,:auj,	MOUSE-X2.DNA	201				240	250	
1923	HUMAN-X2.DNA	201	AAAGCCGGCT	TTGGAAACCT	TGAACGAGAA	TTTTGGTTGG	GCAACGATAA	250
		201	MANGCAGGCT	TTGGAAACCT			GGAACGATAA	250
i den	MOUSE-X2.DNA	251	260		280	290	300	-
	HUMAN-X2.DNA	251	AATTCATCTT	CTGACCAAGA	GTAAGGAAAT	GATTTTGAGA	ATAGATCTTG	300
		231	AATTCATCTT	CTGACCAAGA	GTAAGGAAAT	GATTCTGAGA	ATAGATCTTG	300
:e4	MOUSE-X2.DNA	201	310	320	330	340	350	
-	HUMAN-X2.DNA	301	AAGACTTTAA	TGGTCTCACA	CTTTATGCCT	TGTATGATCA	GTTTTATGTG	350
لينا		201	AAGACTTTAA	TGGTGTCGAA		TGTATGATCA	GTTTTATGTG	350
9	MOUSE-X2.DNA	251	360	370	380	390	400	
l-A	HUMAN-X2.DNA	351	GCTAATGAAT	TTCTCAAATA	CCGATTACAC	ATCGGTAACT	ACAATGGCAC	400
-2		331	GCTAATGAGT	TTCTCAAATA	TCGTTTACAC	GTTGGTAACT	ATAATGGCAC	400
and a	MOUSE-X2.DNA	401	410	420	430	440	450	
J	HUMAN-X2.DNA	401	CGCAGGGGAT	GCCTTGCGTT	TCAGTCGACA	CTACAACCAT	GACCTGAGGT	450
		401	AGCTGGAGAT	GCATTACGTT	TCAACAAACA	TTACAACCAC	GATCTGAAGT	450
Ū	MOUSE-X2.DNA	451	460	470	480	490	500	
·O	HUMAN-X2. DNA	451	TTTTCACAAC	CCCAGACAGA	GACAACGATC	GGTACCCCTC	TGGGAACTGT	500
		421	TTTTCACCAC	TCCAGATAAA		GATATCCTTC	TGGGAACTGT	500
	MOUSE-X2.DNA	501	510	520	530	540	550	
	HUMAN-X2.DNA	201	CCCCCCTATT	ACAGCTCAGG	CTGGTGGTTT	GATTCATGTC	TCTCTGCCAA	550
		301	GGGCTGTACT	ACAGTTCAGG		GATGCATGTC	TTTCTGCAAA	550
	MOUSE-X2.DNA	551	560	570	580	590	600	
	HUMAN-X2. DNA	221	CTTAAATGGC	AAATATTACC	ACCAGAAATA	CAAAGGTGTC	CGTAATGGGA	600
	***************************************	221	CITAAATGGC	AAATATTATC	ACCAAAAATA	CAGAGGTGTC	CGTAATGGGA	600
	MOUSE-X2.DNA	601	610	620	630	640	650	
	HUMAN-X2.DNA	601	TTTTCTGGGG	CACCTGGCCT	GGTATAAACC	AGGCACAGCC .	AGGTGGCTAC	650
	***************************************	801	TTTTCTGGGG	TACCTGGCCT	GGTGTAAGTG	AGGCACACCC	TGGTGGCTAC	650
	MOUSE-X2.DNA	663	660	670	680	690	700	
	HUMAN-X2.DNA	651	AAGTCCTCCT	TCAAACAGGC	CAAGATGATG	ATTAGGCCCA :	AGAATTTCAA	700
		931	AAGICCTCCT	TCAAAGAGGC	TAAGATGATG	ATCAGACCCA /	AGCACTTTAA	700
	MOUSE-X2.DNA		/10	720	730	740	750	
	HUMAN-X2.DNA		GCCATAA	• • • • • • • • • • •	• • • • • • • • • • • • •		• • • • • • • • • •	750
		,01	GCCATAA	• • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • •	• • • • • • • • • •	750

ATCACTCTET TCATTCCTCC AGGTATTGT TATCTARATAG GGCAATTRAT TCCTTCAGCA	10	20	24			
TO			30			
CTTTAGAATA TGCCTTGTTT CATATTTTC ATAGCTARA AATGCCTTGT TTCATATTTT 180 190 200 210 220 230 240 240 250 250 260 270 280 290 300 210 220 230 240 240 250 250 260 270 280 290 300 210 220 230 240 240 250 250 260 270 280 290 300 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250 250						TCCTTCAGCA
130 140 150 160 170 180 TCATAGCTAA ARARTGATGT CTGACGGCTA GGTTCTTATG CTACACAGCA TTTGARATAA 190 200 210 220 230 240 AGCTGARAAA CAATGCATTA TAMAGGAGTC CTTTGTTGTT ATGCCTGTATA CCAATGAACA 310 320 330 340 350 360 ATTGARACT TTTCTATTGC TTGTATTACT TTGCTGTATT TAMAGAATAA TGCTGTATT TAMAGAATAA TGCTGTATT TAMAMATAAT TGTTGGCTGG ATTGARACT TTTCTATTGC TAGTATTACT TCAAGGCAGG CAGATCACTT 400 410 420 GTGTGGAGC TCACGCCTGT AATNCCAGA CTTTGGATG TCAAGGCAGG CAGATCACTT 480 490 400 410 420 GAGGTCAGG GTTTGAGACC AGCCTGGCCA AACATGTAA ACGCTTONN TATTAAAAAT TATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA			J 0			120
TCRTAGCTAA ARARTGATGT CTGACGGCTA GGTTCTATG CTACACACAC TTTGARATAA 190 200 210 220 230 240 AGCTGARARA CAATGCATTT TTAAAGGAGTC CTTTGTTGTT ATGCTGTTAT CCAATGARCA 310 320 330 TACATTAGAT TTTAAATTCT TTTAATTCT TTTAATTCT TTTAATTCT TTTAATTCT TTTAATTACT TTTAATTACT TTTAATTACT TTTTAGCTATT AAAAAAAATAA TGTTGGCTGG 420 430 460 410 420 420 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 590 530 540 540 560 570	130				-	TICATATITY
190 200 210 220 230 240 AGCTGARARA CARTGCATTT TARAGGAGTC CTTTGTTGTT ATGCTGTTATC CCARTGARCA 250 260 270 280 290 300 ATTGCARGCA ATTAGCARTA TTGGAGRATTA TACATTAGAT TACAATTCT TTTAATTCT 310 320 330 340 350 360 ATTGRARCTT TTTCTATTGC TTGTATTACT TGCTGTTATT TGCTGGGGGGGGGG						180
AGCTGARARA CANTGCRTTT TARAGGAGTC CTTTGTTGTT ATGCTGTAT CCARAGAACA 300 290 300 CTTGCARGCA ATTAGCARTA TTGAGRATTA TACATTAGAT TTTACATTCT TTTATTCT TTTATTCT TTGTATTACT TGCTGTATTT AARARATAAT TGTTGGCTGG AARARATAAT TGTTGGCTGG AARARATAAT TGTTGGCTGG CAGATCACTT 480 450 460 410 420 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 590 530 540 580 590 600 600 600 660 660 660 <td>190</td> <td></td> <td>are encountly</td> <td></td> <td></td> <td>TTTGAAATAA</td>	190		are encountly			TTTGAAATAA
250 260 270 280 300 300 300 300 300 300 300 300 300 300 350 360 350 360 350 360 360 350 360 360 350 360 360 350 360 360 360 350 360 360 360 350 360 360 360 360 360 360 360 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 420 <td>AGCTGAAAA</td> <td></td> <td></td> <td></td> <td></td> <td>240</td>	AGCTGAAAA					240
STEGRASCA ATTAGRANTA TTGAGRATTA TACATTAGRAT TTACANTACT TTTACANTACT TTTAC	250					CCAATGAACA
310 320 330 340 350 360 ATTGAAACTT TTTCTATTGC TTGTATTACT TGCTGTATTT AAAAAAATAAT TGTTGGCTGG 370 380 390 400 410 420 GTGTGGTAGC CTCACGCCTGT AATNCCAGCA CTTTGGAATG TCAAGGCAGG CAGATCACTT GAGGTCAGGA GTTTGAGACC AGCCTGGCCA AACATGTGAA ACGCTGTNTN TATTAAAATA ACAAAAATTA GCCGGGCATG GTGGNACATG CCTGTAATCC TAGNTACTTG GGAGGCTGAG GCAGGAGAAT CGCTTGAACC GTGAGAGGAAG AGGTTGCAGT GAGCCAAGAA TGAGCCAACTG GCACTCCAGCA TGGGTGACAG AGAAAACTCT GTCTCAAACA AAAAAAACTCT GTCTCAAACA AAAAAAAAACTCT GTATTTGGC CATGATTTAA AAAAAAAACTCT GTATTTGGC CATGATTTAA AAAAAAAAACTCT GTATTTGGC CATGATTTAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	CTTGCAAGCA					300
ATTGARACTT TITCTATTGC TTGTATACT TGCTGTATTT AMAMATAAT TGTTGGCTGG 370 380 390 400 AMAMATAAT TGTTGGCTGG GTGTGGTAGC TCACGCCTGT AMTNCCAGCA CTTTGGRATG CCAGATCACTT 430 440 450 460 470 480 GAGGTCAGGA GTTTGAGCC AGCCTGGCCA AACATGTGAA ACGCTGTNTN TATTARARAT ACACAGAGAA GCCGGGCATG GTGGAGAGAGA AGGTTGCAGT GAGCCAAGAA TGAGCCACTG GCAGGGGAAT GCGTTGAACC TGAGAGGAAG AGGTTGCAGT GAGCCAAGAA TGAGCCACTG GCACTCCAGCA TGGGTGACAG AGAAAACTCT GTCTCAAACA AAAAAAATAAA AAAAAAAATAAT AAAAAATTATT GCAGTAGGATG GATTTTCACAC AAAGTAAACTCT GTATTTTGGGC CATGATTTAA AAAAAAATAATA AAAAAATTATA AAAAAATTATA AAAAAAATTATA AAAAAAATTATATTTTTGGCC AAAAAAATTATA AAAAAAATTATATTTTTTTTTTTTTTTTTTTTTTTTT	310					TTTAATTTCT
370 380 390 400 410 420	ATTGAAACTT					360
GTGTGGTAGC TCACGCCTGT AATNCCAGCA CTTTGGAATG CAGATCACTT 430 440 450 460 470 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 480 590 540 530 540 550 560 570 580 590 600 600 600 600 600 600 600 660 660 660 660 660 660 660 660 660 660 660 670 710 720 720 780 770 780 770 780 770 780 770 780 860 810	370					TGTTGGCTGG
430 440 450 460 470 480 GRGGTCAGGA GTTTGAGACC AGCCTGGCCA AACATGTGAA ACGCTGTNTN TATTAAAAAT 490 500 510 520 530 540 ACAAAAATTA GCCGGGCATG GTGGNACATG CCTGTAATCC TAGNTACTTG GGAGGCTGAG 550 560 570 580 590 600 GCAGGAGAAT CGCTTGAACC TGAGAGGAAG AGGTTGCAGT GAGCCAAGAA TGAGCCACTG 610 620 630 640 650 660 CACTCCAGCA TGGGTGACAG AGAAAACTCT GTCTCAAACA AAAAAAACTCT AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	GTGTGGTAGC					
GAGGTCAGGA GTTTGAGACC AGCCTGGCCA AACATGTGAA ACGCTGTMN TATTAAAAAT 490 500 510 520 530 540 ACAAAAATTA GCCGGGCATG GTGGNACATG CCTGTAATCC TAGNTACTTG GGAGGCTGAG 550 560 570 580 590 600 GCAGGAGAAT CGCTTGAACC GAGAAAACTCT GAGCCAAGAA TGAGGCCACTG 610 620 630 640 650 660 CACTCCAGCA TGGGTGACAG AGAAAAACTCT GTCTCAAACA AAAAAAAAATAAT AAAATAATAAT AAAAGTAATCT GTATTTTACTT GCACATCTGA 700 710 720 CAGGTATATCA CTCTTTTCAG GCTATAAATTA TTTTGGGTAAT CTTCATTCTG AGACAAAACTT CTTCATTCTG AGACAGAACA ACCCTACAGC ATTTTGGTC CCAACAGGACA ACCCTACAGC ATTTTGGTTC CCAACAGGACA ACCCTACAGC ATTTTGGTTC CCAACAGGACA 880 890 900 GCAATTTAAA TCAACTTGTT CAACAGGACA ACCTTACAC ATTTTGGTTC CCCAAAAAGC	430	· -		-		CAGATCACTT
490 500 510 520 530 540 ACAAAAATTA GCCGGGCATG GTGGNACATG CCTGTAATCC TAGNTACTTG GGAGGCTGAG 550 560 570 580 590 600 GCAGGAGAAT CGCTTGAACC TGAGAGGAAG AGGTTGCAGT GAGCCAAGAA TGAGCCACTG 610 620 630 640 650 660 CACTCCAGCA TGGGTGACAG AGAAAACTCT GTCTCAAACA AAAAATATAAT AAAATTTATT 670 680 690 700 710 720 CAGGTAGATGA CAACAGAACA GTATTTGGGC CATGATTTAA GCACATCTGA 730 740 750 760 770 780 AGGTATATCA CTCTTTTCAG GCTATAATTA CTTCGGTAAT CTTCATTCTG AGACAAACTT 790 800 810 820 830 840 AATCTATATA TCTATATAAT TAAACTTGTT CATTTATCAT TCATGAAATA TAAAATICTT 910 920 930	GAGGTCAGGA				- · •	480
ACARARATTA GCCGGGCATG GTGGNACATG CCTGTAATCC TAGNTACTTG GGAGGCTGAG 550 560 570 580 590 600 GCAGGAGAAT CGCTTGAACC TGAGAGGAAG AGGTTGCAGT GAGCCAAGAA TGAGCCACTG 610 620 630 640 650 660 CACTCCAGCA TGGGTGACAG AGAAAAACTCT GTCTCAAACA AAAAATATAAT AAAATTTATT 670 680 690 700 710 720 CAGGTAGATG GATTCTACAC AAAAGTAATCT GTATTTGGGC CATGATTTAA GCACATCTGA 770 780 AGGTATATCA CTCTTTTCAG GCTATAATTA TTTTGGGTAT CTTCATTCTG AGACAAACTT 780 AATCTATATC ATTTACTTTG ACCCTACAGC ATTTTGGTTC CCAGACTAAG 840 AATCTATATA TCATTAATAT TAAACTTGTT CATTTTATCAT TCATGAAATA TAAAATICTT 910 920 930 940 950 960 GTCATTTAAA ATGTGGTAGC ATAATGTCAC	490					TATTAAAAAT
550 560 570 580 590 600 GCRGGAGAAT CGCTTGAACC TGAGAGGAAG AGGTTGCAGT GAGCCAAGAA TGAGCCACTG 610 620 630 640 650 660 CACTCCAGCA TGGGTGACAG AGAAAACTCT GTCTCAAACA AAAAAAATAAT AAAAATTTATT 670 680 690 700 710 720 CAGTAGGNTG GATTCTACAC AAAGTAATCT GTATTTGGGC CATGATTTAA GCACAACTGA 730 740 750 760 770 780 AGGTATATCA CTCTTTTCAG GCTATAATTA CTTCATTCTG AGACAAACTT 790 800 810 820 830 840 AATCTATATC ATTTACTTTG CAACAGAACA ACCCTACAGC ATTTTGGTTC CCAGACTAAG 850 860 870 880 890 900 GGAACTATATA TCATTTAAAA ATGTGGTAGC ATAATTCAT TCATGAAATA TAAAATTCTT 910 920 930	ACAAAAATTA					540
GCAGGAGAAT CGCTTGAACC TGAGGAGAG AGGTTGCAGT GAGCCAAGAA TGAGCCACTG GAGCCAAGAA TGAGCCACTG GAGCCAAGAA TGAGCCACTG GAGCCAAGAA GAAAAACTCT GTCTCAAACA AAAAAAAAATAAT AAAAATTAATT GCACAATCGA GAGCAACTCGA GAGCCAAGAA AAAAAAAAAAAAAAAAAAAAA	550					GGAGGCTGAG
610 620 630 640 650 660 CACTCCAGCA TGGGTGACAG AGAAAACTCT GTCCAAACA 730 740 750 760 770 780 AGGTATATCA CTCTTTCAG GCTATAATA 750 800 810 820 830 840 AATCTATATC ATTTACTTTG CAACAGAACA ACCCTACAGC 850 860 870 880 890 900 GGAACTAATA TCTATATAT TAAACTTGTT CATTTACTAT TCATGAATA TCATGAAATA TCATGAAACA ATGTGGTAGC ATAATGTCAC 970 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTAAA CCCTACAGC ATTAAACG ATTCAGAAAG ATTCAGAAAG ATTCAGAAAG ATTCAGAAACA ATGTGGTAGC ATAATGTCAC CCCCAAAAAG ATTCAGAAAG ATTCAGAAACA ATGTGGTAGC ATAATGTCAC CCCCAAAAAG ATTCAGAAAG ATTCAGAAAG 1020 960 900 1000 1010 1020	GCAGGAGAAT					600
CACTCCAGCA TGGGTGACAG AGAAAACTCT GTCTCAAACA AAAAAATAAT AAAATTTATT 670 680 690 700 710 720 CAGTAGGNTG GATTCTACAC AAAGTAATCT GTATTTGGGC 770 780 AGGTATATCA CTCTTTTCAG GCTATAATTA TTTGGGTAAT 770 780 AATCTATATC ATTTACTTTG CAACAGAACA ACCCTACAGC 850 840 GGAACTAATA TCTATATAAT TAAACTTGTT CATTTACTAT TCATGAAATA TCATGAAATA TCATGAAATA ATGTGGTAGC ATTAATGTCAC 950 960 GTCATTTAAA CCGTTTAAAA ATGTGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAAG ATTCAGAAAG ATTCAGAAAG ATTCAGAAAG 790 960 GTCATTTAAA CCGTTTAAAA ATGTGGTAGC ATAATGTCAC CCCCAAAAAGC ATTCAGAAAG ATTCAGAAAAG ATTCAGAAAAG ATTCAGAAAAG ATTCAGAAAAG ATTCAGAAAAG ATTCAGAAAAG ATTCAGAAAAAG ATTCAGAAAAAG ATTCAGAAAAAAAAAG ATTCAGAAAAAAAAAA	610					TGAGCCACTG
670 680 690 700 710 720 CAGTAGGNTG GATTCTACAC AAAGTAATCT GTATTTGGGC 730 740 750 760 770 780 AGGTATATCA CTCTTTCAG GCTATAATA TTTGGGTAAT 790 800 810 820 830 840 AATCTATATC ATTTACTTTG CAACAGAACA ACCCTACAGC ATTTTGGTC CCAGACTAAG 850 860 870 880 890 900 GGAACTAATA TCTATATAAT TAAACTTGTT CATTTACTAT TCATGAATA TCATGAATA TCATGAATA ATGTGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAGA 790 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTAAA CTCATGAAGA CCCCAAAAAGC ATTCAGAAAGC ATTCAGAAAAGC ATTCAGAAAGC ATTCAGAAAAGC ATTCAGAAAAAGC ATTCAGAAAAGC ATTCAGAAAAAGC ATTCAGAAAAAGC ATTCAGAAAAAGC ATTCAGAAAAAAAAAGAAAAAAAAAA	CACTCCAGCA					
CAGTAGGNTG GATTCTACAC AAAGTAATCT GTATTTGGGC CATGATTTAA GCACATCTGA 730 740 750 760 770 780 AGGTATATCA CTCTTTTCAG GCTATAATTA TTTGGGTAAT CTTCATTCTG AGACAAACTT 790 800 810 820 830 840 AATCTATATC ATTTACTTTG CAACAGAACA ACCCTACAGC ATTTTGGTTC CCAGACTAAG 850 860 870 880 890 900 GGAACTAATA TCTATATAAT TAAACTTGTT TCATTAAATA TAAACTTGTT TCATGAAATA TAAAATI.CTT 910 920 930 940 950 960 GTCATTTAAA ATGTGGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAAG 970 980 990 1000 1010 1020	670	,		·		AAAATTTATT
730 740 750 760 770 780 AGGTATATCA CTCTTTTCAG GCTATAATTA TTTGGGTAAT CTTCATTCTG AGACAAACTT 790 800 810 820 830 840 AATCTATATC ATTTACTTG CAACAGAACA ACCCTACAGC ATTTTGGTTC CCAGACTAAG 850 860 870 880 890 900 GGAACTAATA TCTATATAAT TAAACTTGTT CATTATCAT TCATGAAATA TCATGAAATA TCATGAAATA TCATGAAATA TAAACTTGTT CATTATAAA CCGTTTAAAA ATGTGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAAG 970 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTAAAA CCCTATAAAA CCCTAAAAAGC ATTCAGAAAGC CAATGTAACT GTGAAGACCA GGGTTTAAAA CCCTATAAAA CCCTATAAAAGC ATTCAGAAAGC CAATGTAAACT GTGAAGACCA GGGTTTAAAA CCCTATAAAA CCCTATAAAA CCCCAAAAAGC ATTCAGAAAGC CAATGTAAACT GTGAAGACCA GGGTTTAAAA CCCTATAAAA CCCTATAAAAC TAAACTAGAAAGC CAATGTAAACT GTGAAGACCA GGGTTTAAAA CCCTATAAAAC CAATGTAAAC TAAACTAGAAAGC ATTCAGAAAGC CAATGTAAACT GTGAAGACCA GGGTTTAAAA CCCTATAAAA CCCTATAAAACT TAAAATTCAGAAAGC CAATGTAAACT GTGAAGACCA GGGTTTAAAA CCCTATAAAA CCCTATAAAAC CAATGTAAACT TAAAATTCAGAAAGC CAATGTAAACT CAATGTAAAACT CAATGTAAAAACT CAATGTAAAACT CAATGTAAAACT CAATGTAAAACT CAATGTAAAACT CAATGTAAAACT CAATGTAAAAAACT CAATGTAAAAACT CAATGTAAAAAAACT CAATGTAAAAACT CAATGTAAAAACT CAATGTAAAAAAAAACT CAATGTAAAAAAAAAA	CAGTAGGNTG					720
AGGTATATCA CTCTTTTCAG GCTATAATTA TTTGGGTAAT CTTCATTCTG AGACAAACTT 790 800 810 820 830 840 AATCTATATC ATTTACTTG CAACAGAACA ACCCTACAGC ATTTTGGTTC CCAGACTAAG 850 860 870 880 890 900 GGAACTAATA TCTATATAAT TAAACTTGTT CATTTATCAT TCATGAAATA TAAAATI.CTT 910 920 930 940 950 960 GTCATTTAAA ATGTGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAAG 970 980 990 1000 1010 1020 CAATGTAACT GGGTTTBAAC CTTCATTCAGAAATA ATTCAGAAAG ATTCAGAAAG	730					GCACATCTGA
790 800 810 820 830 840 AATCTATATC ATTTACTTTG CAACAGAACA ACCCTACAGC ATTTTGGTTC CCAGACTAAG 850 860 870 880 890 900 GGAACTAATA TCTATATAAT TAAACTTGTT CATTTATCAT TCATGAAATA TCATATAAAA ATGTGGTAGC ATTATCAT TCATGAAAAA CCCTAAAAA ATGTGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAAG 970 980 990 1000 1010 1020	AGGTATATCA					780
### AATCTATATC ATTTACTTTG	790	. –				AGACAAACTT
850 860 870 880 890 900 GGAACTAATA TCTATATAAT TAAACTTGTT CATTTATCAT TCATGAAATA TAAAATICTT 910 920 930 940 950 960 GTCATTTAAA ATGTGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAAG 970 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTTAAAC CTAACACAC CTAACACACACACACACACACACACACACACACACACAC	AATCTATATC					840
GGAACTAATA TCTATATAAT TAAACTTGTT CATTTATCAT TCATGAAATA TAAAATICTT 910 920 930 940 950 960 GTCATTTAAA CCGTTTAAAA ATGTGGTAGC ATAATGTCAC CCCAAAAAGC ATTCAGAAAG 970 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTAAAC CTAAAAGC ATTCAGAAAG	850			-		CCAGACTAAG
910 920 930 940 950 960 GTCATTTANA CCGTTTANA ATGTGGTAGC ATAATGTCAC CCCAAAAGC ATTCAGAAG 970 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTANAC CTAATGTCAC	GGAACTAATA					
GTCATTTANA CCGTTTANA ATGTGGTAGC ATAATGTCAC CCCANANAGC ATTCAGANAG 970 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTANAG CTANAGACCA CCCANANAGC ATTCAGANAG	910					Taaaati.ctt
970 980 990 1000 1010 1020 CAATGTAACT GTGAAGACCA GGGTTTTAACC	GTCATTTAAA					
CAATGTAACT GTGAAGACCA GGGTTTTAAAG CTAATGTAACT GTGAAGACCA GGGTTTTAAAG CTAATGTAACT 1010 1020	970			-	•	ATTCAGAAAG
THE PERSON WITH THE PERSON WITH THE PERSON OF THE PERSON O	CAATGTAACT					
1030 1040 1070	1030					AACTCCTTAG
ATGTTTGATG TTGAAAACTG CTTTAACATG AA	ATGTTTGATG				1070	1080

3'UTR of hfgl2. The A at position 1 corresponds to position 1354 on the cDNA.

<u>5/24</u>

			10	٠				
	MOUSEPRO.AMI	1			•		•	
	HUMANPRO.AMI		PREPGALNA			ERASTOAA		50
		1	M-4-10-10-1			KDERNKDV	VRIMESRAR	50
	MOUSEPRO AMI		60					
			-GSOME LI		M	EVRTLKEAVD	SLKKSCODCK	100
	HUMANPRO.AMI	51	EAGE	LEPLTHOLE K	FSRIDOVF	EVONEKEIVN		100
			110	120	130	140	150	. 100
	MOUSEPRO.AMI	101	LOADDHRDPG	GNGGN	GAETAELSRV			150
	HUMANPRO.AMI	101	LOADDNeDPG		APGEVGUNRV	RELESEVNKE	SSELKNANGE	
			160	170	180			150
	MOUSEPRO.AMI	151	IQGLQ GRUET	LHLVNMNNIE	NYVDNKVANL		200	
	HUMANPRO.AMI		INVLHERIEK		NYVDSKVANL			200
and James			210	220	230		ESKCPSOEOI	200
	MOUSEPRO.AMI	201)S@PVOHLIY	KDCSDHYVL		240	250	
pm.	HUMANPRO. AMI	201	DSRPVOHLIY		RRSSGAYRVT		YCDMETMGGG	250
		201	260	KDCSDYTAI	KRSSETYRVT	PUPKNSSFEV	YCDMETMGGG	250
ingranc ingranc	MOUSEPRO.AMI	251		270	280	290	300	
N.	HUMANPRO.AMI		WTVLQARLDG		YKAGEGNLEP	EFWLGNDK1H	LLTKSKEMIL.	300
e de	HOLDER PRO . MAI	251	#TVLQARLDG	STRETPTACE	YKAGFGNLRP	EFWLGNDKIH	LLTKSKEMIL	300
	WOUGDDD		310	320	330	340	- 350	
W	MOUSEPRO.AMI		RIDLEDFNGL	TLYALYDOFY	VANEFLKYRL	HIGNYNGTAG	DALRESEHYN	350
я	HUMANPRO.AMI	301	RIDLEDENGV	BLYALYDOFY			DALRENKHYN	350
-6			360	370	380	390	400	330
	MOUSEPRO.AMI	351	HDLREFTTPD	RDNDRYPSGN	CGLYYSSGWW		SKYYHOKYKE	
-L	HUMANPRO.AMI	351						400
india.		,	410	420	430		SKYYHOKYRS	400
Jī	MOUSEPRO.AMI	401				440	450	
₫	HUMANPRO. AMI	!				MIRPKNEKE	• • • • • • • • • •	450
, Pa		301	VINIOITWOIN	PGVSEAHPGG	YKSSFK <mark>B</mark> AKM	MIRPRHERP*	• • • • • • • • • •	450

			10	20) 3(0 40	50	
	MOUSEPRO.AMI	1	MRLPGWLWLS	SAVLAACR-A	VEEHNLTEG		ARLEGSGRCE	50
	HUMANPRO.AMI	1	MKLANWYWLS	SAVLATYGFI	VVANNETEE	KDERAKDVCE	VRLESRGKCE	50
			60	70				30
	MOUSEPRO.AMI	51	-GSQCPFQLT	LPTLTIQLPR	OLGSMEEVLE		SLKKSCQDCK	100
	HUMANPRO.AMI	51	EAGECPYQVS	LPPLTIQLPK	OFSRIEEVE	EVONLKETVN	SLKKSCODCK	100
			110	120				100
	MOUSEPRO.AMI	101	LQADDHRDPG	GNGGN			SSELKNAKDQ	150
	HUMANPRO.AMI	101	LQADDNGDPG	RNGLLLPSTG	APGEVGDNRV	RELESEVNKT.	SSELKNAKEE	150
			160	170				150
	MOUSEPRO.AMI	151	IQGLQGRLET	LHLVNMNNIE			CSKCPSQEHM	200
	HUMANPRO.AMI	151	INVLHGRLEK	LNLVNMNNIE	NYVDSKVANI	TFVVNSLDGK	CONCLUCENT	200
			210	220	230		250	200
324	MOUSEPRO.AMI	201	QSQPVQHLIY	KDCSDHYVLG		PDHRNSSFEV	VCDMETMCCC	252
	HUMANPRO.AMI	201	QSRPVQHLIY	KDCSDYYAIG	KRSSETYRVT	PDPKNSSFEV	VCDMETMCCC	250
F			260	270	280		300	250
im:	MOUSEPRO.AMI	251	WTVLQARLDG			EFWLGNDKIH	TIMPOPPATE	
4 1	HUMANPRO.AMI	251	WTVLQARLDG	STNFTRTWOD	YKAGFGNI.BR	EFWLGNDKIH	TOTASVEMIT	300
			310	320	330	340	350	300
	MOUSEPRO.AMI	301	RIDLEDFNGL			HIGNYNGTAG	330	
E	HUMANPRO.AMI	301	RIDLEDFNGV	ELYALYDOFY	VANEFI.KYRI.	HVGNYNGTAG	DALBESKHIN	350
4			360	370	380	390		350
i	MOUSEPRO.AMI	351	HDLRFFTTPD			FDSCLSANLN	400	
mile.	HUMANPRO.AMI	351	HDLKFFTTPD	KONDRYPSCH	CCI VVCCCW	FDACLSANLN	GKYYHQKYKG	400
eni:			410	420	430			400
-i-	MOUSEPRO.AMI	401		PGINQAQPGG		440	450	
n	HUMANPRO.AMI	401	VRNGIFWGTW	PGVSENUDGG	TUSSEVÕVV	MIRPKHFKP*	• • • • • • • • • • • • • • • • • • • •	450
# # ###,				LGVJDARFGG	INSSEREARM	WIKEKHEKE.	• • • • • • • • • •	450

7/24

		10 LSSAVI.	20 ATYGELUU	30	40	50	60	7
HELIX	KKhhhhhh	hhhhhh	<i>PPPPPPPP</i>	інирурунинин Імиропет (СТКС	ERAKDVCPVRL	esrgkczem	eecb agast bi	PLTIQLE
SHEET	333333	535535	38883331	.mnnnnnee				t
TURN			TTTT		22222		33325551	**55:
COIL			****	IIII		IIIIIII	TITI T	TT TT
					С	. cc	CC	
		80	90	100	110	120	130	
	OFSRIEEV	Prevon	ilkeivhsi	KKSCODCKLO	addhgdpgrhg	LLLPSTGA	GEVChuuvori	14
	***************************************	uvuuru	MARKER					ihhhh Seseand
SHEET	*******	22222				3 S 3		HHAM
TORN COIL	T		III	TITITITI 1	***************************************	I IIIIIII	TITITIT	
								CC
		50	160	170	180	190	200	21
1700 014	SSELKNAK	eeinvi	HCRLEKL)	ilvroni en	VDSKVANLTFV	VNSLDGKCS	KCPSOEOIOSI	e e Revout. 1
KELIX			minimizati (1)	munn	րրրրեր	hhh	hhhhhh	
SHEET TURN		S S Ss			32222E e	SSa	.323333	
COIL	cc		TTTT	TITI	TITIT	TTTTTT		
	_	20	230	240	250	260	270	26
HELIX	KDCSDYYX	igkrss	ETYRVTPL	PKNSSFEVYC	DHETHGGGWTV	Loarldgst	NETRTHODYKI	40 AGPGN7.5
SHEET	_			•	h hhh	հեհե	hhhH.	HH
		_	\$55 55	33335	5552 255	3355s	3 5 533	,116
COIL	IIIIIII	IIIII	TI III	TITTIT	TITTITI	TITTI	TI TITT	
							d	cccc
		90	300	310	320	330	340	94
	EFWLGHDK	IHLLIK	SKEMILRI	DLEDFNGVE	YALYDOFYVAN	FFT KYDT LIS	GNYNGTAGOA 1	35
	•••		հիկներեր	ւեկկրբերեր	հիհիհիհիհի	hhhH		or use:
oneet Turn	1783	55553	55555	3S3	38888888888	55555551		
COIL	TITIT	TT	TI	TITT			TITITITI	1111
							cc	CC C
	-	60	370	380	390	400	410	44
	HDLKFFTT	PDKDND	RYPSGNC	TLYYSSGWWFT	ACLSANLHGRY	YHOKYRGUI	NGT FNGTHOG	42
	հերերեր			hhi	hhlih			MKHH MKHH
SHEET	*****			a\$a s\$\$	SS:	2888888a		
Sh eet Turn			TITTTTT	asa asa Tittii	· · -	35555531 T		
SHEET			TTTTTTT		issa Titititt		essssssss TT TTT	
Sh eet Turn	III I	777777 30	440		· · -			
SHEET TURN COIL	TTT T	TTITTI 30 10041RE	440		· · -			
SHEET TURN COIL HELIX	TTT T	777777 30	440		· · -			
SHEET TURN COIL HELIX FHEET	TTT T 4 YKSSEKEA bbilli	TTTTTT 30 100MIRE KHMH 888	440 PKHFKP*		· · -			
SHEET TURN COIL HELIX	TTT T	TTTTTT 30 100MIRE KHMH 888	440		· · -			

<u>8/24</u>

			1	.0 2	20 3		•	
	MOUSEPRO.DNA		-	-		0 4	0 50 G TAGGAGCCCG	
	HUMANPRO.DNA		1 TAGGGTTGG	A AGCCAGGTC	M CCTCACEAN	C CCLCLLCL	A TACAGTCATG	50
			6		0 8	_	_	50
	MOUSEPRO.DNA	5	_	- ,			0 100 A ATTCTTCATA	
	HUMANPRO.DNA	5	1 GAAGTGTAA	A GAGTCTGCC	A DENTANGEC	G TGTCTGACA	A ATTCTTCATA A GGATTTGGC-	100
			11	0 12		_	_	100
	MOUSEPRO.DNA	10					0 150 T TTCTATAGGA	
	HUMANPRO.DNA	10	TA-AAATTA	A CCCIIIGON	C ACLARAGE	G TATAGGTTA	TTCTATAGGA	150
			16	0 UGGGATATA		_	A GGTTAAAGAC	150
	MOUSEPRO. DNA	151				19	200	
	HUMANPRO. DNA	151	ATAAATATG	- ULICUMULI	C CTTGTGCAC	G-GTAACAG	CATGAAGGCT	200
			210	22			ATAAAACATT	200
	MOUSEPRO. DNA	201		-		240	250	
1000	HUMANPRO. DNA	201	TAGATTT	TOCCCARCE	r ATGTCCAGTT	GGAGACAGT	CCAGGGCCAA	250
Ū			260) 16CCCA1G1(C A-GTCATTT			250
Ë	MOUSEPRO. DNA	251				290	300	
	HUMANPRO. DNA	251	AAAACCC	TICICAGAT	A GAAAGTGCGC	CTGCCTGCCC	-TGCTCTGAG	300
IJ			310	. IIIIIAAACI	A AGAAATCTTA			300
i indi math	MOUSEPRO. DNA	301					350	
	HUMANPRO. DNA	301	CALATTION	GAGAGIAGI	CAGTTA	GAATTAAGAG	GCAGTAGAGA	350
		***	360	CONCOLOGIA	TCTCTAACTG			350
أيذ	MOUSEPRO. DNA	351				390	400	
Eş	HUMANPRO. DNA	351	CTTCAGCCTC	TCARCACA	GTTAGAGA	TATAAATATG	AGAACTGGAC	400
			410	1 GAAGAGAAA	GTTAGAAAAC		AATGCTACAT	400
-4	MOUSE PRO. DNA	401				440	450	
-4	HUMANPRO. DNA	401	GTTTTCA-AC	ACACCIGIGA	TCTCTGTGTT	TAGGAGGGAG	AGGCAGAGAG	450
J		.01	460		ACCAAGTGGC		AGGTAGAAGA	450
Ð	MOUSEPRO. DNA	451		470		490	500	
Ē	HUMANPRO. DNA	451	ACCACCC	CAAGGCCAGC	CTGAGCTACT	TGAGACCCAG	TCTAAATAAA	500
:5:45		.02	510	IGGAGACAGA	AAGCAA		CCTGCCAGGG	500
	MOUSEPRO. DNA	501		520		540	550	
	HUMAN PRO. DNA	501	CTACCTCCAC	ALLACAGAGT	GCCTTTAACT	AGTACAGAGA	AAGAATTTGG	550
			560	AA-AGAAAGG	GCAAAGATGC		AGAAGTTCAG	550
	MOUSE PRO. DNA	551		570	580	590	600	
	HUMAN PRO. DNA	551	GACAGACACT	CCCA . TR. C	CTGAAATAAT	TTTTAAGTAA	TAAAATCCCT	600
			610	GGCATA-G	CTCAAA-GAT		GCAGC	600
	MOUSEPRO. DNA	601		620	630	640	650	•
	HUMAN PRO. DNA	601	TGTGGAAGAT	CACACTACA	G-GTCAGTAT	GCACAATGAA	CTTAAGAGAG	650
		•••	660		TTACCAAAAT		CAAAGGAG	650
	MOUSEPRO. DNA	651		670	680	690	700	
	HUMAN PRO. DNA	651	GCAGCT	ACTCCOMM	GTGATGGGGA	AGGACAGCCA	CTGCCTGTGA	700
			710	720	-TGATGA		TGTCCTTT	700
	MOUSE PRO. DNA	701		720	730	740	750	
	HUMAN PRO. DNA	701	TAAATGGGTC	TTACACACACTOC	AAGTGTTTTA	ACCACTGACG	ATTACATAGC	750
			760	TINGACATTT	AGACATTAT		ATGCTACGGA	750
	MOUSE PRO. DNA	751		770	780	790	800	
	HUMAN PRO . DNA	751	CAAAGCAAT-	AGB B ACTRAC	AGCCGTATTC	TCTGCCAGTT	CTCTTCCCTT	800
			810	ODATORADOR	A-CTTTTTC			800
	MOUSE PRO . DNA	801 '		820 ATGAGAGAGA	830	840	850	
	HUMANPRO. DNA	801 1	TTTCAACTAC	TCAACAGACA	CACACAGAGA	ATCCATTTAA	AGAGCGGACC	850
		~~*	860	AAAJUMMU	AGT-CAACTG			850
			8 0 0	870	880	890	900	

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FIGURE 8 cont'd

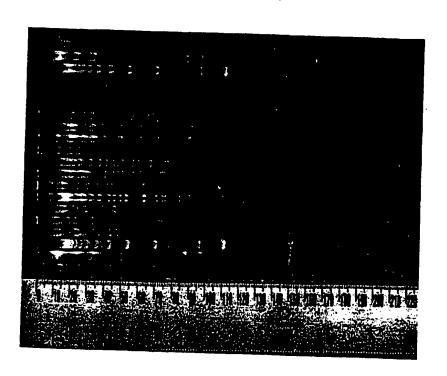
	MOUSEPRO. DNA	05	1 7777					
	HUMANPRO. DNA	0.5	1 TITGTTCTG	A TTAGGGGCA	A TTTTAAGTA	C TTAAGAGTT	C ACACAAAGTC	900
		. 65	1 IIIGITACA	C TTAGAAACT	T CTAAAAGTG	C TTAAGATTT	C ACCTGAAAGT	900
	MOUSEPRO.DNA		91	U 92	0 93	0 94	050	
	HUMANPRO. DNA	90.	TAGCCTTCA	A AAAGAAAAC	A GGTTCCCAA	ACTA	GGGAGGAAA	950
		90.	L CCAACAT-G	a agaaaatac	A GGCTCCCA	A TGCCCCATT	C TAAGAAGAAA	950
	MOUSEPRO. DNA		961	97(98	0 00	1000	
	HUMANPRO. DNA	95.	CAGAATCAT	r TCCATTTTG(G TGACATTTA-	- GTGGGAAGA	GCTCACAGAC	1000
		95.	AAGGACCAT	TTCATTTTAC	TAACGTTTC:	r Gttctatag	CAGTTTGGAT	1000
	MOUSEPRO.DNA		1010	1020	1036	1046	1050	-555
	HUMANPRO. DNA	1001	ATTTAGACGI	TCCAACTCT1	TCCCCACTAC	G TG	ACCAAGT-AT	1050
		1001	AACTAGCTCT	TACTTTTAI	CTTTAAAAA	TGTTTTTCC	GTGAAGTTAC	1050
	MOUSEPRO.DNA		1060	1070	1080	1000		-000
	HUMANPRO. DNA	1021	ATAATATGGT	' ATCTTTTGGG	CACTGGTATT	ACAA-CTGTT	TTTTAAACAA	1100
्रकृतका स्थान	THE TOTAL	1051	GIAIAATTAT	TTACTTCAAG	CG-TAGTATA	CCAAATTACT	TTAGAAATGC	1100
i Ç am	MOUSEPRO. DNA		1110	1120	1130	1140	1150	-100
	HUMANPRO. DNA	1101	AAGACTTTCC	TTGTGCTTTA	CTARARAC-C	CA-GACGGTG	AATCTTGAAT	1150
-1	· · · · · · · · · · · · · · · · · · ·	1101	ANGACITITE	TTATACTTCA	TAAAATACAT	TATGAAAGTG	AATCTTGT	1150
-	MOUSEPRO. DNA		1160	1170	1180	1190	1200	1150
	HUMANPRO. DNA	1151	ACAATGCGTG	GCACCCACGG	CAGGCATTCT	ATTGTGCATA	GTTTTGACTG	1200
a		1151	IGGCIGIGIA	CATTTGACTA	TAATAATTTC	AATGCATATT	ATTTCTATTG	1200
-A	MOUSEPRO. DNA		1210	1220	1230	1240	1250	-200
led.	HUMANPRO. DNA	1201	ACAGGAGATG	ACAGCATTTG	GCTGGCTGCG	CTTGCTGAGG	ACCCTCTCCT	1250
-L		1201	AGAGTAAGTT	ACAGITTITG	GCAAACTGCG	TTTGATGAGG	GCTATCTCCT	1250
J	MOUSEPRO. DNA		1260	1270	1280	1200	1200	
14 1 . 174	HUMANPRO. DNA	1251	CCTG-TGTG-	GCGTCTGAGA	CT-GTGATGC	AAATGCGCCC	GCCCTTTTCT	1300
		1231	CIICCIGIGC	GTTTCTAAAA	CTTGTGATGC	AAACGCTCCC	ACCCTTTCCT	1300
Ü	MOUSEPRO. DNA		1310	1320	1330	1340	1250	2200
	HUMANPRO. DNA	1301	GGGAACTCAG	AACGCCTGAG	TCAGGCGGCG	GTGGCTATTA	AAGCG	1350
		1301	GGGAACACAG	AAAGCCTGAC	TCAGGCCATG	GCCGCTATTA	AAGCAGCTCC	1350
	MOUSEPRO. DNA		1360	1370	1380	1200		1330
	HUMANPRO. DNA	1321	CCTGGTC	AGGCT	GGGCT-GCCG	CACTGCAAGG	ATG	1400
	- IV DIM	1331	AGCCCTGCGC	ACTCCCTGCT	GGGTGAGCAG	CACTGTAAAG	ATG	1400

.			-	
TACCCTTCC	U 2	0 30	40	50
I AUGUL 1 I G	AAGUUAGGTC -	TCCTGAGTATO	CGAGAATAAA	TACAGTCATG
61 GAACTCTAA	0 7	0 80	90	100
GAAGIGIAA	AGAGICIGCO	AACATTTTGAC	SAATGTGAATA(
111	12	0 130	140	150
AAAA I TAAGO	SGGATATACA	GAAAAGTCAT <u>A</u>	GGAAATCAGG	TTAAAGACAT
	'	TCF1 F	PEA3	
161	17)	180	190	200
ARAIAIGAGA	LAGGCTACA	GAGIGITITAA	GTAATACAATA	AAACATTTA
216	TAL	NF	IL6 240	
CATTTTTCC	22)	230	240	250
ONITITIECE	CAIGICAGT	LATTITGAAAT	OAAATTTTAAT.	CAAAAAAAC
260	270	NE ITP	290	
CCTTTTTAAA	,	, 280 TTXTCXCXTC	290	300
A A ARRE	CANCHHAIC.	I TA I GAGA [G]	CAATATGCAAA	ACAAATTAA
31	0 32	0 330	340	350
AAGGAGGTG	GTTTCTCTAA	CTGAAGCTGT	CCTCTTTCCT	GCCTTCAGCC
TCF1				
36	0 37	0 386	390	400
TCTGAAGAG.	aaagttagaa	AACTATTATC	ATTAATGCTAC	ATGTTTTGAA
		NF_E1		
	0 42		440	450
CAAGCTGAT		GCCCAGAGAG	CAGGTAGAAGA	ACCAGCGTGG
. شد م	PHTH	_		
461	U 47	0 480	490	500
AGACAGAAA	GUAAGAGGCC	CGCCTGCCAG	GCTACCTGCA	<u>GAAAG</u> AAAGG
*	o		NF :	IL6
510	U 52	0 530) 54n	550
UCAAAGATG(LIGTAGGCAA	GAGAAGTTCAC	GACAGACACT	GCATAGCTC
TCF1	n ==			
561			590	600
TCF1			TGACAGTACA	ATTACCAAAA
ICFI		HLH		
611		2Å		
				650
• OI CURROU!	TCF1	CAGCTACTGGT	TTETGATGAAA	JACAATTATG
660	·	0 680	NF ILE	
			690 CATTTATATAC	700
710	72	0 730		
			CTCCACTAGT:	750
TCF1		ACCACIIIII	CICCACIAGI.	HUHUHUT
761	0 77	0 780	790	800
		AAAGTCAACTO	CAATAGTCAG	UUD ○⊀™≎™Э∆&&
	T	CF1 bHLH		ARGC101RC
		E SHEET (RUL	Æ 26)	
		•	•	

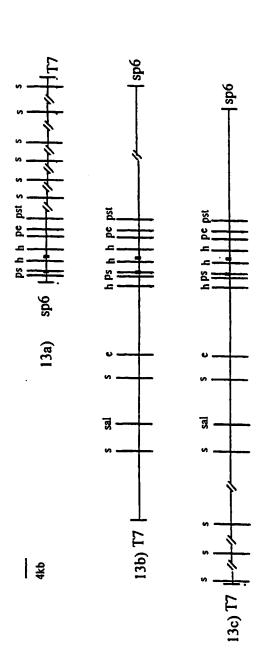
FIGURE 9 CONT'D

	820	830	840	850.
TTTGTTACACT	TAGAAACTT	CTAAAAGTGC	TTAAGATTTC	ACCTCALACC
		TCF1		bhih
	870	880	0.00	000
CCAACATGAAC	SAAAATACAG	GCTCCCAAT	・ プログラン・ファック・ファック・ファック・ファック・ファック・ファック・ファック・ファック	900
910	920	930	940	
AGGACCATTTT	CATTTTAGT	'AACGTTTCTG	טאַנ הגהגדארתTT	950
960	970	980	990	
ACTAGCTCTTA	CTTTTTATO	ΟΟΟ ΤΤΥΑΑΑΑΥΤΤ	╵ ╱┸┸┸┸┸┸┸	1000
1010	1020	1030	GITTTTCCAG	
TATAATTATTT		こことではないない	1040	1050
	MOTICANGC	GIAGIAIACC	AAAI TACTTT	AGAAATGCAA
1060	1070	1000		F IL6
	U / U I	1080	1090	1100
GACTTTTCTTA	IACTICATA	AAATACA <u>TTA</u>	<u>TGAAAG</u> TGAA	TCTTGTTGGC
		NF	IL6	
111U	1120	1130	1140	1150
TGTGTACATTT	GACTATAAT.	AATTTCAATG	CATATTATTT	CTATTGAGAG
DHTH				
1160	1170	1180	1190	1200
IAAGITACAGT	TTTTGGCAA	ACTGCGTTTG.	ATGAGGGCTA'	ICTCCTCTTC
1210	1220	1230	1240	1250
CTGTGCGTTTC	TAAAACTTG	IGATGCAA:AC	CTCCCACCC	TTTCCTCCCx
		AABS		- 1 1 CC 1 GGGA
	1270	1280	1290	1200
ACACAGAAACG	CIGACTCAGO	CACCTCCCC	TATTAAACC	1300
+1	AP 1	bhlh	TATA box	AGC I CLACE
1310	1320	1330:	HAIN DOX	
CTGCGCACTCC	TGCTGGGT	∷∪∪∪ ∂⊄∂∆⊜C∂	CT A A A CATO	
		-mochoche I (HAARGAIG	

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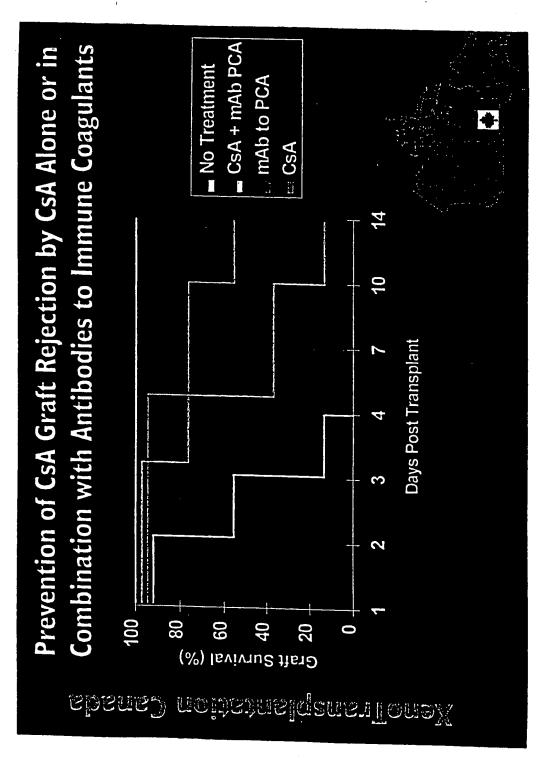






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SUBSTITUTE SHEET (RULE 26)

15/24 FIGURE 13

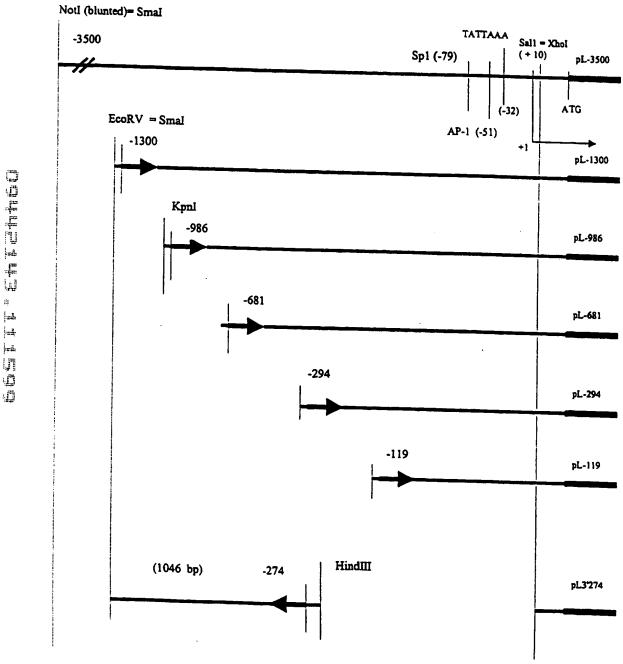
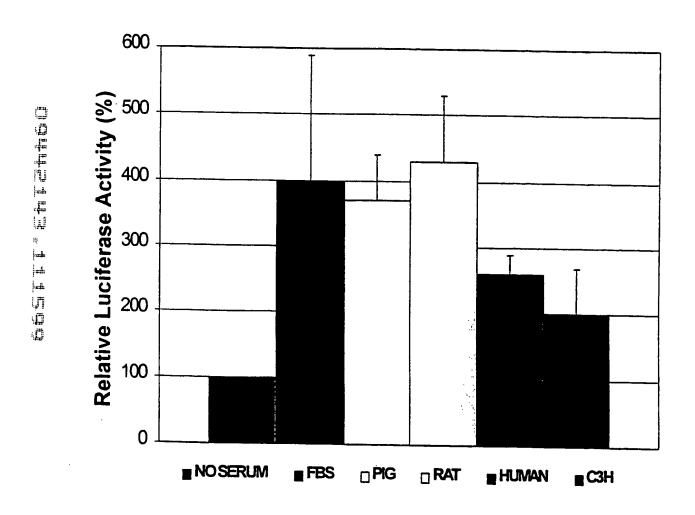


FIGURE 14



17/24 FIGURE 15

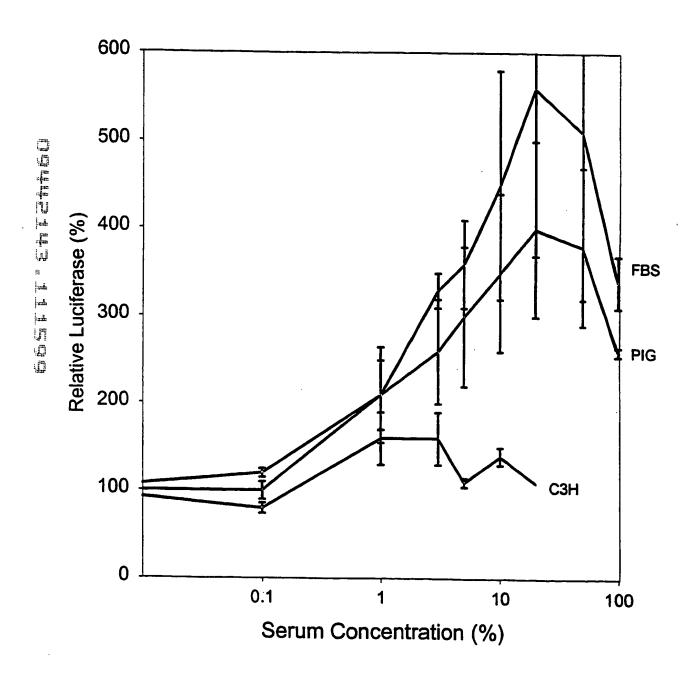


FIGURE 16

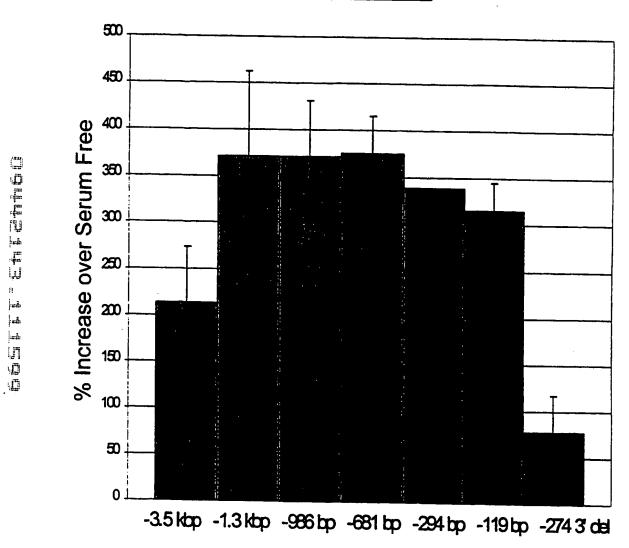
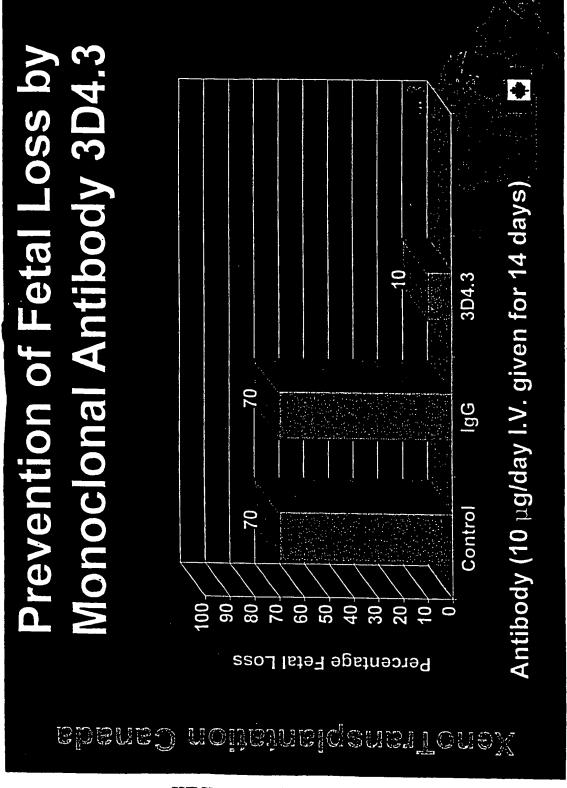


FIGURE 17

5'- CCAAGTATAT AATATGGTAT CTTTTGGGCA CTGGTATTAC AACTGTTTT -270
TAAACAAAAG ACTTTCCTTG TGCTTTACTA AAAACCCAGA CGGTGAATCT -220
TGAATACAAT GCGTGGCACC CACGGCAGGC ATTCTATTGT GCATAGTTTT -170
GACTGACAGG AGATGACAGC ATTTGGCTGC GTGCGCTTGC TGAGGACCCT -120
CTCCTCCTGT GTGGCGTCTG AGACTGTGAT GCAAATGCGC CCGCCCTTTT -70
CTGGGAACTC AGAANGCCTG AGTCAGGCGG CGGTGGCTAT TAAAGCGCCT -20
GGTCAGGCTG GGCTGCCGCA CTCCAAGG-3'

FIGURE

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h postinfection

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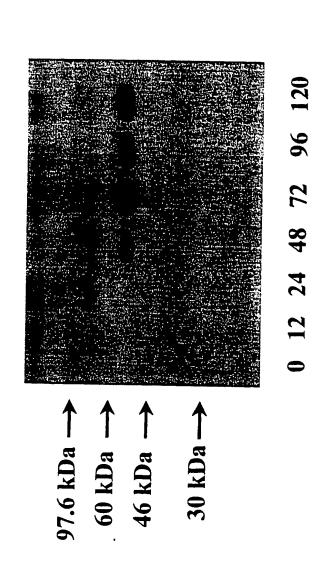


FIGURE 19

The lanes are:

H5 + wild type virus 1. H5cells

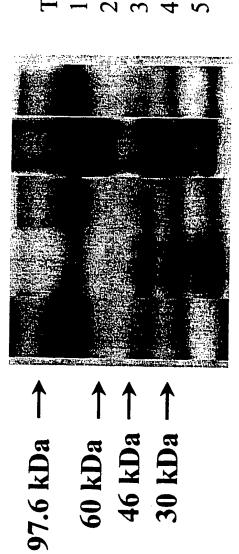
H5 + recombinant

97.6 kDa 60 kDa

The lanes are:
1. H5cells
2. H5 + wild type virus
3. H5 + recombinant
virus

97.6 kDa →
60 kDa →
46 kDa →

FIGURE 22



The lanes are:

1. ¹²⁵I-Prothrombin (PT)

PT +RVV + Factor X
PT +H5
PT + H5-RV
PT + purified protein (3 μg)